

## SEQUENCE LISTING

&lt;110&gt; Merck &amp; Co., Inc.

&lt;120&gt; Antigen-Binding Proteins Targeting

S. Aureus ORF0657n

&lt;130&gt; 22319Y PCT

&lt;150&gt; 61/007,998

&lt;151&gt; 2007-12-17

&lt;150&gt; 60/932,788

&lt;151&gt; 2007-05-31

&lt;160&gt; 54

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mAb CS-D7 light chain

&lt;400&gt; 1

Glu	Ile	Val	Met	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Val	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Tyr	Val	Ser	Asp	Asn
		20						25					30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile
	35						40					45			
Tyr	Gly	Ala	Ser	Thr	Arg	Ala	Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Ser
65					70					75				80	
Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Asn	Trp	Arg	Pro
			85						90					95	
Val	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala
			100					105					110		
Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser
		115					120					125			
Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu
	130					135					140				
Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser
145					150					155				160	
Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu
				165					170					175	
Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val
			180					185					190		

Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys
		195					200					205			
Ser	Phe	Asn	Arg	Gly	Glu	Cys									
	210					215									

&lt;210&gt; 2

&lt;211&gt; 456

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mAb CS-D7 heavy chain

&lt;400&gt; 2

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Arg	Ser	Ser
			20					25					30		
Ser	Tyr	Tyr	Trp	Gly	Trp	Phe	Arg	Gln	Thr	Pro	Gly	Lys	Gly	Leu	Glu
		35					40					45			
Trp	Leu	Gly	Asn	Val	Phe	Phe	Ser	Gly	Ser	Ala	Tyr	Tyr	Asn	Pro	Ser
	50					55					60				
Leu	Lys	Asn	Arg	Val	Thr	Ile	Ser	Ile	Asp	Thr	Ser	Glu	Asn	Gln	Ser
65					70				75						80
Ser	Leu	Lys	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Pro	Gln	Ala	Tyr	Ser	His	Asp	Ser	Ser	Gly	His	Ser	Pro
			100					105					110		
Phe	Asp	Leu	Trp	Gly	Arg	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser
		115					120					125			
Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr
	130					135						140			
Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro
145					150					155					160
Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val
				165					170					175	
His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser
			180					185					190		
Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile
		195					200					205			
Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val
	210					215					220				
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
225					230					235					240
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
				245					250					255	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
			260					265					270		
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
		275					280					285			
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
	290					295					300				
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
305					310					315					320

```

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
      325                      330          335
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
      340                      345          350
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
      355                      360          365
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
      370                      375          380
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
385      390                      395          400
Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
      405                      410          415
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
      420                      425          430
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
      435                      440          445
Ser Leu Ser Leu Ser Pro Gly Lys
      450                      455

```

<210> 3  
 <211> 112  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-E11 light chain variable region

```

<400> 3
Gln Ala Val Leu Thr Gln Pro Ser Ser Val Ser Gly Ala Pro Gly Gln
 1          5          10          15
Arg Val Thr Ile Ser Cys Thr Gly Asp Arg Ser Asn Ile Gly Ala Thr
      20          25          30
Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly Arg Ala Pro Lys Leu
      35          40          45
Leu Ile Tyr Gly Asn His Asn Arg Pro Ser Gly Val Pro Glu Arg Phe
      50          55          60
Ser Gly Ser Lys Ser Gly Ser Ser Ala Ser Leu Ala Ile Ala Gly Leu
65      70      75      80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Gly
      85          90          95
Leu Ser Gly Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu Gly
      100         105         110

```

<210> 4  
 <211> 126  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-E11 heavy chain variable region

&lt;400&gt; 4

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Arg	Ser	Ser
			20					25					30		
Ser	Tyr	Tyr	Trp	Gly	Trp	Phe	Arg	Gln	Thr	Pro	Gly	Lys	Gly	Leu	Glu
		35					40					45			
Trp	Leu	Gly	Asn	Val	Phe	Phe	Ser	Gly	Ser	Ala	Tyr	Tyr	Asn	Pro	Ser
	50					55					60				
Leu	Lys	Asn	Arg	Val	Thr	Ile	Ser	Ile	Asp	Thr	Ser	Glu	Asn	Gln	Ser
65					70					75					80
Ser	Leu	Lys	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Pro	Gln	Ala	Tyr	Ser	His	Asp	Ser	Ser	Gly	His	Ser	Pro
			100					105					110		
Phe	Asp	Leu	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120					125			

&lt;210&gt; 5

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mAb CS-C10 light chain variable region

&lt;400&gt; 5

Gln	Ala	Val	Leu	Thr	Gln	Pro	Ser	Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln
1				5					10					15	
Arg	Val	Thr	Ile	Ser	Cys	Thr	Gly	Gly	Ser	Ser	Asn	Ile	Gly	Ala	Gly
			20					25					30		
Tyr	Asp	Val	His	Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Thr	Ala	Pro	Lys	Leu
		35					40					45			
Leu	Ile	Tyr	Gly	Asn	Ser	Asn	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe
	50					55					60				
Ser	Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu
65					70					75					80
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Ser	Ser
			85						90				95		
Leu	Asn	Gly	Pro	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Val	Thr	Val	Leu
			100					105					110		

Gly

&lt;210&gt; 6

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; mAb CS-C10 heavy chain variable region

```

<400> 6
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1          5          10          15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Arg Ser Ser
      20          25          30
Ser Tyr Tyr Trp Gly Trp Phe Arg Gln Thr Pro Gly Lys Gly Leu Glu
      35          40          45
Trp Leu Gly Asn Val Phe Phe Ser Gly Ser Ala Tyr Tyr Asn Pro Ser
      50          55          60
Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Glu Asn Gln Ser
      65          70          75          80
Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
      85          90          95
Cys Ala Arg Pro Gln Ala Tyr Ser His Asp Ser Ser Gly His Ser Pro
      100          105          110
Phe Asp Leu Trp Gly Arg Gly Thr Met Val Thr Val Ser Ser
      115          120          125

```

```

<210> 7
<211> 108
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> mAb CS-A10 light chain variable region

```

```

<400> 7
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1          5          10          15
Thr Ala Thr Ile Thr Cys Ser Gly Asp Asn Leu Gly Asp Lys Ser Val
      20          25          30
Ser Trp Tyr Gln Gln Lys Ala Gly Gln Ser Pro Val Leu Val Met Ser
      35          40          45
Gln Gly Ser Lys Arg Pro Leu Gly Ile Pro Asp Arg Ile Ser Gly Ser
      50          55          60
Asn Ser Gly Thr Thr Ala Thr Leu Thr Ile Ser Gly Val Gln Thr Val
      65          70          75          80
Asp Glu Ala Asp Phe Tyr Cys Gln Thr Trp Asp Arg Tyr Thr Gly Val
      85          90          95
Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
      100          105

```

```

<210> 8
<211> 126
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> mAb CS-A10 heavy chain variable region

```

```

<400> 8
Arg Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
 1          5          10          15

```

Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Arg	Ser	Ser
			20					25					30		
Ser	Tyr	Tyr	Trp	Gly	Trp	Phe	Arg	Gln	Thr	Pro	Gly	Lys	Gly	Leu	Glu
		35					40					45			
Trp	Leu	Gly	Asn	Val	Phe	Phe	Ser	Gly	Ser	Ala	Tyr	Tyr	Asn	Pro	Ser
	50					55					60				
Leu	Lys	Gly	Arg	Val	Thr	Ile	Ser	Ile	Asp	Thr	Ser	Glu	Asn	Gln	Ser
65					70					75					80
Ser	Leu	Lys	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Pro	Gln	Ala	Tyr	Ser	His	Asp	Ser	Ser	Gly	His	Ser	Pro
			100					105					110		
Phe	Asp	Leu	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		115					120					125			

<210> 9  
 <211> 111  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb BMV-H11 light chain variable region

Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1				5					10					15	
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
			20					25					30		
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
		35					40					45			
Met	Ile	Tyr	Glu	Gly	Ser	Lys	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
	50					55					60				
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
65					70					75					80
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ser	Ser	Tyr	Thr	Thr	Arg
				85					90					95	
Ser	Thr	Arg	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	
			100					105					110		

<210> 10  
 <211> 128  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb BMV-H11 heavy chain variable region

Arg	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Ile	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Ser
			20					25						30	

Ser	Tyr	Tyr	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu
		35					40					45			
Trp	Ile	Gly	Asn	Met	Phe	Tyr	Ser	Gly	Gly	Ala	Tyr	Tyr	Asn	Pro	Ser
	50					55					60				
Leu	Lys	Ser	Arg	Val	Ser	Ile	Ser	Val	Gly	Pro	Ser	Ser	Asn	Gln	Phe
65					70					75				80	
Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Pro	Leu	Gly	Tyr	Asn	Phe	Asp	Ser	Ser	Gly	Gln	Gly	Lys
			100					105					110		
Ser	Ala	Phe	Glu	Ile	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115					120					125			

<210> 11  
 <211> 111  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb BMV-E6 light chain variable region

Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1				5					10					15	
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
			20					25					30		
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
		35					40					45			
Met	Ile	Tyr	Glu	Gly	Ser	Lys	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
	50					55					60				
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
65					70					75					80
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ser	Ser	Tyr	Thr	Thr	Arg
				85					90					95	
Ser	Thr	Arg	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	
			100					105					110		

<210> 12  
 <211> 128  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb BMV-E6 heavy chain variable region

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Ser
			20					25					30		
Ser	Tyr	Tyr	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu
		35					40					45			

Trp	Ile	Gly	Asn	Met	Phe	Tyr	Ser	Gly	Ser	Ala	Tyr	Tyr	Asn	Pro	Ser
50						55				60					
Leu	Lys	Ser	Arg	Val	Ser	Ile	Ser	Val	Gly	Pro	Ser	Ser	Asn	Gln	Phe
65					70					75					80
Ser	Leu	Lys	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Pro	Leu	Gly	His	Asn	Phe	Asp	Ser	Ser	Gly	Gln	Gly	Glu
			100					105					110		
Gly	Ala	Phe	Glu	Ile	Trp	Gly	Arg	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
	115						120					125			

<210> 13  
 <211> 111  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb BMV-D4 light chain variable region

Gln	Ser	Val	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1				5					10					15	
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
			20				25						30		
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
		35					40					45			
Met	Ile	Tyr	Glu	Gly	Ser	Lys	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
50						55					60				
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
65					70					75					80
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ser	Ser	Tyr	Thr	Thr	Arg
				85					90					95	
Ser	Thr	Arg	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	
			100					105					110		

<210> 14  
 <211> 128  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb BMV-D4 heavy chain variable region

Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Ser
			20					25					30		
Ser	Tyr	Tyr	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu
		35					40					45			
Trp	Ile	Gly	Asn	Met	Phe	Tyr	Ser	Gly	Gly	Ala	Tyr	Tyr	Asn	Pro	Ser
50						55					60				



Leu	Lys	Asn	Arg	Val	Ser	Ile	Ser	Val	Gly	Pro	Ser	Ser	Asn	Gln	Phe
65					70				75					80	
Ser	Leu	Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Pro	Leu	Gly	Tyr	Asn	Phe	Asp	Ser	Ser	Gly	Gln	Gly	Lys
			100					105					110		
Ser	Ala	Phe	Glu	Ile	Trp	Gly	Lys	Gly	Thr	Met	Val	Thr	Val	Ser	Ser
		115					120					125			

<210> 15  
 <211> 111  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb BMV-C2 light chain variable region

Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Ala	Ala	Pro	Gly	Gln
1				5					10					15	
Lys	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Thr	Ser	Asn	Ile	Gly	Asn	Asn
			20					25					30		
Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Met
		35					40					45			
Ile	Tyr	Asp	Val	Ser	Lys	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser
	50					55					60				
Gly	Ser	Lys	Ser	Gly	Asn	Ser	Ala	Ser	Leu	Asp	Ile	Ser	Gly	Leu	Gln
65					70					75					80
Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Ala	Ala	Trp	Asp	Asp	Ser	Leu
				85					90					95	
Ser	Glu	Phe	Leu	Phe	Gly	Thr	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	
			100					105					110		

<210> 16  
 <211> 128  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb BMV-C2 heavy chain variable region

Glu	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu
1				5					10					15	
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Gly	Ser	Ile	Ser	Ser	Ser
			20					25					30		
Ser	Tyr	Tyr	Trp	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu
		35					40					45			
Trp	Ile	Gly	Asn	Met	Phe	Tyr	Ser	Gly	Ser	Ala	Tyr	Tyr	Asn	Pro	Ser
	50					55					60				
Leu	Lys	Ser	Arg	Val	Ser	Ile	Ser	Val	Gly	Pro	Ser	Ser	Asn	Gln	Phe
65					70					75					80

Ser	Leu	Lys	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Pro	Leu	Gly	His	Asn	Phe	Asp	Ser	Ser	Gly	Gln	Gly	Glu
			100					105					110		
Gly	Ala	Phe	Glu	Ile	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115					120					125			

<210> 17  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-D7 VL CDR1

<400> 17  
 Arg Ala Ser Gln Tyr Val Ser Asp Asn Leu Ala  
 1 5 10

<210> 18  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-D7 VL CDR2

<400> 18  
 Gly Ala Ser Thr Arg Ala Thr  
 1 5

<210> 19  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-D7 VL CDR3

<400> 19  
 Gln Gln Tyr Asn Asn Trp Arg Pro Val Thr  
 1 5 10

<210> 20  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-E11 VL CDR1

<400> 20  
Thr Gly Asp Arg Ser Asn Ile Gly Ala Thr Tyr Asp Val His  
1 5 10

<210> 21  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> mAb CS-E11 VL CDR2

<400> 21  
Gly Asn His Asn Arg Pro Ser  
1 5

<210> 22  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> mAb CS-E11 VL CDR3

<400> 22  
Gln Ser Tyr Asp Ser Gly Leu Ser Gly Tyr Val  
1 5 10

<210> 23  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> mAb CS-D10 VL CDR1

<400> 23  
Thr Gly Gly Ser Ser Asn Ile Gly Ala Gly Tyr Asp Val His  
1 5 10

<210> 24  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> mAb CS-D10 VL CDR2

<400> 24  
Gly Asn Ser Asn Arg Pro Ser  
1 5

<210> 25  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-D10 VL CDR3

<400> 25  
 Gln Ser Tyr Asp Ser Ser Leu Asn Gly Pro Val Val  
 1 5 10

<210> 26  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-A10 VL CDR1

<400> 26  
 Ser Gly Asp Asn Leu Gly Asp Lys Ser Val Ser  
 1 5 10

<210> 27  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-A10 VL CDR2

<400> 27  
 Gln Gly Ser Lys Arg Pro Leu  
 1 5

<210> 28  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb CS-A10 VL CDR3

<400> 28  
 Gln Thr Trp Asp Arg Tyr Thr Gly Val Val  
 1 5 10

<210> 29  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAbs BMV-H11, BMV-E6 and BMV-D4 VL CDR1

<400> 29  
 Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser  
 1 5 10

<210> 30  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAbs BMV-H11, BMV-E6 and BMV-D4 VL CDR2

<400> 30  
 Glu Gly Ser Lys Arg Pro Ser  
 1 5

<210> 31  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAbs BMV-H11, BMV-E6 and BMV-D4 VL CDR3

<400> 31  
 Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val  
 1 5 10

<210> 32  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> mAb BMV-C2 VL CDR1

<400> 32  
 Ser Gly Ser Thr Ser Asn Ile Gly Asn Asn Tyr Val Ser  
 1 5 10

<210> 33  
 <211> 7  
 <212> PRT

<213> Artificial Sequence

<220>

<223> mAb BMV-C2 VL CDR2

<400> 33

Asp Val Ser Lys Arg Pro Ser  
1 5

<210> 34

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> mAb BMV-C2 VL CDR3

<400> 34

Ala Ala Trp Asp Asp Ser Leu Ser Glu Phe Leu  
1 5 10

<210> 35

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> mAbs CS-D7, CS-E11, CS-D10 and CS-A10 VH CDR1

<400> 35

Gly Gly Ser Ile Arg Ser Ser Ser Tyr Tyr Trp Gly  
1 5 10

<210> 36

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mAbs CS-D7 and CS-E11 VH CDR2

<400> 36

Asn Val Phe Phe Ser Gly Ser Ala Tyr Tyr Asn Pro Ser Leu Lys Asn  
1 5 10 15

<210> 37

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mAbs CS-D7, CS-E11, CS-D10 and CS-A10 VH CDR3

<400> 37

Pro	Gln	Ala	Tyr	Ser	His	Asp	Ser	Ser	Gly	His	Ser	Pro	Phe	Asp	Leu
1				5					10					15	

<210> 38

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mAb CS-D10 VH CDR2

<400> 38

Asn	Val	Phe	Phe	Ser	Gly	Ser	Ala	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 39

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mAb CS-A10 VH CDR2

<400> 39

Asn	Val	Phe	Phe	Ser	Gly	Ser	Ala	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Gly
1				5					10					15	

<210> 40

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> mAbs BMV-H11, BMV-E6, BMV-D4 and BMV-C2 VH CDR1

<400> 40

Gly	Gly	Ser	Ile	Ser	Ser	Ser	Ser	Tyr	Tyr	Trp	Gly
1				5					10		

<210> 41

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mAb BMV-H11 VH CDR2

<400> 41

Asn	Met	Phe	Tyr	Ser	Gly	Gly	Ala	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 42

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> mAbs BMV-H11 and BMV-C2 VH CDR3

<400> 42

Pro	Leu	Gly	Tyr	Asn	Phe	Asp	Ser	Ser	Gly	Gln	Gly	Lys	Ser	Ala	Phe
1				5					10					15	
Glu Ile															

<210> 43

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mAbs BMV-E6 and BMV-C2 VH CDR2

<400> 43

Asn	Met	Phe	Tyr	Ser	Gly	Ser	Ala	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 44

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> mAb BMV-D4 VH CDR2

<400> 44

Asn	Met	Phe	Tyr	Ser	Gly	Gly	Ala	Tyr	Tyr	Asn	Pro	Ser	Leu	Lys	Asn
1				5					10					15	

<210> 45

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> mAbs BMV-E6 and BMV-C2 VH CDR3



&lt;400&gt; 45

Pro	Leu	Gly	His	Asn	Phe	Asp	Ser	Ser	Gly	Gln	Gly	Glu	Gly	Ala	Phe
1				5					10					15	
Glu Ile															

&lt;210&gt; 46

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; consensus sequence of SEQ ID NOs: 35 and 40

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 5

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 46

Gly	Gly	Ser	Ile	Xaa	Ser	Ser	Ser	Tyr	Tyr	Trp	Gly
1				5				10			

&lt;210&gt; 47

&lt;211&gt; 645

&lt;212&gt; PRT

&lt;213&gt; Staphylococcus aureus

&lt;400&gt; 47

Met	Asn	Lys	Gln	Gln	Lys	Glu	Phe	Lys	Ser	Phe	Tyr	Ser	Ile	Arg	Lys
1				5					10					15	
Ser	Ser	Leu	Gly	Val	Ala	Ser	Val	Ala	Ile	Ser	Thr	Leu	Leu	Leu	Leu
		20						25					30		
Met	Ser	Asn	Gly	Glu	Ala	Gln	Ala	Ala	Ala	Glu	Glu	Thr	Gly	Gly	Thr
		35					40					45			
Asn	Thr	Glu	Ala	Gln	Pro	Lys	Thr	Glu	Ala	Val	Ala	Ser	Pro	Thr	Thr
	50					55					60				
Thr	Ser	Glu	Lys	Ala	Pro	Glu	Thr	Lys	Pro	Val	Ala	Asn	Ala	Val	Ser
65				70						75				80	
Val	Ser	Asn	Lys	Glu	Val	Glu	Ala	Pro	Thr	Ser	Glu	Thr	Lys	Glu	Ala
			85						90					95	
Lys	Glu	Val	Lys	Glu	Val	Lys	Ala	Pro	Lys	Glu	Thr	Lys	Ala	Val	Lys
		100						105					110		
Pro	Ala	Ala	Lys	Ala	Thr	Asn	Asn	Thr	Tyr	Pro	Ile	Leu	Asn	Gln	Glu
	115					120						125			
Leu	Arg	Glu	Ala	Ile	Lys	Asn	Pro	Ala	Ile	Lys	Asp	Lys	Asp	His	Ser
	130				135						140				
Ala	Pro	Asn	Ser	Arg	Pro	Ile	Asp	Phe	Glu	Met	Lys	Lys	Glu	Asn	Gly
145				150					155					160	
Glu	Gln	Gln	Phe	Tyr	His	Tyr	Ala	Ser	Ser	Val	Lys	Pro	Ala	Arg	Val
			165					170						175	
Ile	Phe	Thr	Asp	Ser	Lys	Pro	Glu	Ile	Glu	Leu	Gly	Leu	Gln	Ser	Gly
			180					185					190		

Gln	Phe	Trp	Arg	Lys	Phe	Glu	Val	Tyr	Glu	Gly	Asp	Lys	Lys	Leu	Pro
		195					200					205			
Ile	Lys	Leu	Val	Ser	Tyr	Asp	Thr	Val	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg
	210					215					220				
Phe	Ser	Val	Ser	Asn	Gly	Thr	Lys	Ala	Val	Lys	Ile	Val	Ser	Ser	Thr
225					230					235					240
His	Phe	Asn	Asn	Lys	Glu	Glu	Lys	Tyr	Asp	Tyr	Thr	Leu	Met	Glu	Phe
				245					250					255	
Ala	Gln	Pro	Ile	Tyr	Asn	Ser	Ala	Asp	Lys	Phe	Lys	Thr	Glu	Glu	Asp
			260					265					270		
Tyr	Lys	Ala	Glu	Lys	Leu	Leu	Ala	Pro	Tyr	Lys	Lys	Ala	Lys	Thr	Leu
		275					280					285			
Glu	Arg	Gln	Val	Tyr	Glu	Leu	Asn	Lys	Ile	Gln	Asp	Lys	Leu	Pro	Glu
	290					295					300				
Lys	Leu	Lys	Ala	Glu	Tyr	Lys	Lys	Lys	Leu	Glu	Asp	Thr	Lys	Lys	Ala
305					310					315					320
Leu	Asp	Glu	Gln	Val	Lys	Ser	Ala	Ile	Thr	Glu	Phe	Gln	Asn	Val	Gln
				325					330					335	
Pro	Thr	Asn	Glu	Lys	Met	Thr	Asp	Leu	Gln	Asp	Thr	Lys	Tyr	Val	Val
			340					345					350		
Tyr	Glu	Ser	Val	Glu	Asn	Asn	Glu	Ser	Met	Met	Asp	Thr	Phe	Val	Lys
		355					360					365			
His	Pro	Ile	Lys	Thr	Gly	Met	Leu	Asn	Gly	Lys	Lys	Tyr	Met	Val	Met
	370					375					380				
Glu	Thr	Thr	Asn	Asp	Asp	Tyr	Trp	Lys	Asp	Phe	Met	Val	Glu	Gly	Gln
385					390					395					400
Arg	Val	Arg	Thr	Ile	Ser	Lys	Asp	Ala	Lys	Asn	Asn	Thr	Arg	Thr	Ile
				405					410					415	
Ile	Phe	Pro	Tyr	Val	Glu	Gly	Lys	Thr	Leu	Tyr	Asp	Ala	Ile	Val	Lys
			420					425					430		
Val	His	Val	Lys	Thr	Ile	Asp	Tyr	Asp	Gly	Gln	Tyr	His	Val	Arg	Ile
		435					440					445			
Val	Asp	Lys	Glu	Ala	Phe	Thr	Lys	Ala	Asn	Thr	Asp	Lys	Ser	Asn	Lys
	450					455					460				
Lys	Glu	Gln	Gln	Asp	Asn	Ser	Ala	Lys	Lys	Glu	Ala	Thr	Pro	Ala	Thr
465					470					475					480
Pro	Ser	Lys	Pro	Thr	Pro	Ser	Pro	Val	Glu	Lys	Glu	Ser	Gln	Lys	Gln
				485					490					495	
Asp	Ser	Gln	Lys	Asp	Asp	Asn	Lys	Gln	Leu	Pro	Ser	Val	Glu	Lys	Glu
			500					505					510		
Asn	Asp	Ala	Ser	Ser	Glu	Ser	Gly	Lys	Asp	Lys	Thr	Pro	Ala	Thr	Lys
		515					520					525			
Pro	Thr	Lys	Gly	Glu	Val	Glu	Ser	Ser	Ser	Thr	Thr	Pro	Thr	Lys	Val
	530					535						540			
Val	Ser	Thr	Thr	Gln	Asn	Val	Ala	Lys	Pro	Thr	Thr	Ala	Ser	Ser	Lys
545					550					555					560
Thr	Thr	Lys	Asp	Val	Val	Gln	Thr	Ser	Ala	Gly	Ser	Ser	Glu	Ala	Lys
				565					570					575	
Asp	Ser	Ala	Pro	Leu	Gln	Lys	Ala	Asn	Ile	Lys	Asn	Thr	Asn	Asp	Gly
			580					585					590		
His	Thr	Gln	Ser	Gln	Asn	Asn	Lys	Asn	Thr	Gln	Glu	Asn	Lys	Ala	Lys
		595					600					605			
Ser	Leu	Pro	Gln	Thr	Gly	Glu	Glu	Ser	Asn	Lys	Asp	Met	Thr	Leu	Pro
	610					615					620				

Leu Met Ala Leu Leu Ala Leu Ser Ser Ile Val Ala Phe Val Leu Pro  
 625 630 635 640  
 Arg Lys Arg Lys Asn  
 645

<210> 48  
 <211> 105  
 <212> PRT  
 <213> Homo sapien

<400> 48  
 Gln Pro Lys Ala Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu  
 1 5 10 15  
 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 20 25 30  
 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val  
 35 40 45  
 Lys Ala Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys  
 50 55 60  
 Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
 65 70 75 80  
 His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
 85 90 95  
 Lys Thr Val Ala Pro Thr Glu Cys Ser  
 100 105

<210> 49  
 <211> 19  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> heavy chain leader

<400> 49  
 Met Glu Trp Ser Trp Val Phe Leu Phe Phe Leu Ser Val Thr Thr Gly  
 1 5 10 15  
 Val His Ser

<210> 50  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> light chain leader

<400> 50  
 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr  
 1 5 10 15

Asp Ala Arg Cys  
20

<210> 51  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide primer

<400> 51  
acagatgccca gatgcgaaat tgtgatgaca cagtct 36

<210> 52  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide primer

<400> 52  
tgcagccacc gtacgtttaa tctccagtcg tgtccc 36

<210> 53  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide primer

<400> 53  
acaggtgtcc actcgcaggt gcagctgcag gagtcg 36

<210> 54  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide primer

<400> 54  
gcccttggtg gatgcactcg agacggtgac cagggt 36